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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 12/18/02
Searcher: _____
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
____ STIC
____ CM-1
____ Pre-S
Type of Search
____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors
____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 12, 2002, 08:24:07 ; Search time 2 Seconds
(without alignments)
1.464 Million cell updates/sec

Title: us-09-371-347a-2
Perfect score: 3624
Sequence: 1 MRRFLLYATGQGAIAIE.....AMKTLATLKEEKRYLDIWS 698

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.1
Ygapop 10.0, Ygapext 0.1
Fgapop 6.0, Fgapext 0.1
Delop 6.0, Delext 0.1

Searched: 1 seqs, 2097 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:

-MODE=frame-p2n model -DEV=soft -Q=us-09-371-347a-2 -DB=us-09-371-347a-1
-SUFFIX=pro -OUT=align_2_1 -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -OCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pro
-NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : us-09-371-347a-1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3624	100.0	2097	1	us-09-371-347a-1

ALIGNMENTS

RESULT 1
us-09-371-347a-1

Alignment Scores:

Pred. No.: 0 Length: 2097
Score: 3624.00 Matches: 698
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

us-09-371-347a-2 (1-698) x us-09-371-347a-1 (1-2097)

QY 1 MRRFLLYATGQGAIAIE.....AMKTLATLKEEKRYLDIWS 20
DB 1 ATGAGGAGGTTCTGTACTATATGCTACACAGGAGGACGCAAGGCCATTCGAGAA 60

QY 21 G L U M E C Y S G L U G L N A l a V a l H i S G l y P h e S e r A l a S p l e u H i S C y S I l e S e r G l u 40
DB 61 G A A A T G T G T G A C A A C C T G T G A C T G A T T T T T C G C A G A T C T T C A C T G A T T A C T G A A 120
QY 41 S e r A s p l y s T y r A s p l e u y s T h r G l u T h r A l a P r o l e u V a l V a l S e r T h r 60
DB 121 T C C G A T A A G A T A C C T A A A A C C G A A C A G C T C C T G T T G T T G T T C G T T C A C A G 180
QY 61 G l y T h r G l y A s p P r o P r o A s p T h r A l a a r g l y s P h e V a l l y S c l u l l e g l n s n g l n t h r 80
DB 181 G G C A C C G A G A C C A C C C A C A C A G C C C A G A T T G T T A A G A A A T A C A A C C A A A C A 240
QY 81 L e u P r o V a l A s p P h e A l a H i S l e A r g T y r G l y L e u l e u g l y S p s e r G l u 100
DB 241 C T G C G G T T G A T T C T T T G C T C A C T G C C G G T A G G T T A C T G G C T T C G G T A C A A 300
QY 101 T y r T h r T y r P h e C y s a n g l y l y s l e i l e a s p l y s a r g l e u g l n l e u g l y a l a 120
DB 301 T A C A C C T A C T T T G C A A T G G G G A G A T A A T G A T A A C G A C T T C A A G A G C T T G A G C C 360
QY 121 A r g H i s P h e T y r A s p T h r G l y H i S l a a s p A s p C y s V a l G l y L e u l e u V a l I g l u 140
DB 361 C G C A T T T C T A T G A C A C T G A C A T G C A G A T G A C T G T G A G T T A C A C T T G T G T T G A G 420
QY 141 P r o T r i P l e A l a g l y L e u T P P r o A l a l e u A r g l y S H i S P h e a r g s e r A r g l y G l n 160
DB 421 C C G T G A T T G C T G A C T T G G C C A C C C T C A G A A C A T T T T A G C T A A G A G A C A A 480
QY 161 G l u G l u l l e S e r G l y A l a l e u P r o V a l A l a S e r P r o A l a S e r L e u a r T T h r A s p l e u a l 180
DB 481 G A G A G A T A A G T G C C A C C C C G A T C C C G T G C A T C A C T G A C C T T G A G A C A G A C C T T G T G 540
QY 181 L y s S e r G l u l e u l e u H i S l e g l u S e r G l n V a l G l u l e u a r g P h e a s p s e r G l y 200
DB 541 A A C T C A G A C T G T G A C A T T G A A T C A A G T C A G A C C T T C G A T T C A T G T T C A G A 600
QY 201 A r g l y A s p s e r G l u V a l l e u l y S g l n A l a V a l A s s e r a n g l n s e r A n V a l 220
DB 601 A G A A G A T T C T A G A G T T T T G A A G C A A A A T G C A G T A C A C A C C A A T C C A A T G T T G A 660
QY 221 I l e g l u A s p P h e g l u S e r L e u T h r A r g S e r V a l P r o P r o l e u S e r G l n A l a S e r L e u 240
DB 661 A T T G A G A C A T T T A G T C C T A C C A C T T A C C C G T C G G T A C C C A C T T C A C A A G C C T C T G 720
QY 241 A s n l l e P r o g l y l e u P r o P r o g l u T y r l e u g l n V a l H i S l e u g l n l u S e r l e u g l n 260
DB 721 A A T A T T C T G G T T T A C C C C C A G A A T A T T T A C A G T A C A C T G C A G A G T C T T G G C C A G 780
QY 261 G l u l u S e r G l n V a l S e r V a l T h r S e r A l a a s p P r o V a l P h e g l n V a l P r o l l e S e r l y s 280
DB 781 G A G A A A G C A A T A C T G A C T T G A C T T C A G C A G A T C C A G T T T T C A A G T C C A A T T T C A A G 840
QY 281 A l a V a l G l n l e u T h r T h r A s n A s p A l a l l e l y s T h r L e u l e u V a l G l u l e u a s p l e 300
DB 841 G C A G T T C A C T T A C T A C G A A T G A T G C C A T A A A A C C A C T C T G T G T A G A A T T G A C A A T T 900
QY 301 S e r A s n T h r A s p P h e s e r T y r G l n P r o g l y A s p A l a P h e s e r V a l l e c y s P r o A n S e r 320
DB 901 T C A A A T A C A G A C T T T C T A T A G C C T G A G A T G C C T T C A G C T G A T T G C C C T A A C A G T 960
QY 321 A s p S e r G l V a l G l n S e r L e u l e u g l n A r g l e u g l n l e u g l u s p l y s A r g l u H i S C y S 340
DB 961 G A T T C G A G T A C A A G C C T A C T C C A A A G A C T C A C A C T T G A A G A T A A A G A G A G C A C T G C 1020
QY 341 V a l l e u l e u l y l l e l y s A l a a s p T h r l y s l y S g l y A l a T h r L e u P r o g l n H i S l e 360
DB 1021 G T C C T T T T G A A A T A A A G A G A C A C A A G A A G A A G A G A C T T A C C C C A G A T A A 1080
QY 361 P r o A l a G l y C y s s e r L e u g l n P h e l l e P h e T h r T r p C y s l e u g l u l l e a r g A l a l l e P r o 380
DB 1081 C C T G C G G A T G T T C T C C A G T T C A T T T T A C C T G T G T C T T G A A A T C C G A G A A A T T C C T 1140

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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 12, 2002, 08:25:56 ; Search time 2 Seconds
(without alignments)
1.464 Million cell updates/sec

Title: us-09-371-347a-42
Perfect score: 3623
Sequence: 1 MRRFLLYATQCGAKAIAE.....AMKTLATLKEEKRYLDIWS 698

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1 seqs, 2097 residues
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL=frame_plus.p2n.model -DEV=soft -Q=us-09-371-347a-42 -DB=us-09-371-347a-41
-SUFFIX=pro -OUT=align_42_41 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pro
-NORM-ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXX
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : us-09-371-347a-41:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3623	100.0	2097	1	us-09-371-347a-41

ALIGNMENTS

RESULT 1
us-09-371-347a-41
ALIGNMENT Scores:
Pred. No.: 0
Score: 3623.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 1
Gaps: 0

us-09-371-347a-42 (1-698) x us-09-371-347a-41 (1-2097)

QY 1 MetArgArgGheuleuleuLeuTYrAlaThGInGInGInAlaAlaAlaAlaAlaGlu 20
DB 1 ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGACAGGCAAGGCCATCGCAGAA 60

QY 21 GluIleCysGluGlnAlaValAlaHisGlyPheSerAlaAspLeuHisCysIleSerGlu 40
DB 61 GAAATATGTGAGACAGCTGTGTACATGCAATTTTCTGCAATCTTACTGTATTAATGCAA 120
QY 41 SerAspLysTYrAspLeuYstrGlrThrAlaProLeuValAlaValSerThrThr 60
DB 121 TCGGATTAAGATGACCTAAACCGAAGAGCTCCCTGTTGTGTGTTCTTACACAG 180
QY 61 GlyThrGlyAspProProAspThrAlaArgLysPheValLysGluIleGlnAsnGlnThr 80
DB 181 GGCACCGGAGACCCACCCGACACGCCGCAAGCTTTGTAAGCAAAATACAGAACCAACA 240
QY 81 LeuProValAspPhePheAlaHisIleuArgTYrGlyLeuLeuGlyLeuGlyAspSerGlu 100
DB 241 CTGCGGTTGATTTCTTGTCTACCTGCGGTATGGTTACTGGGCTCCGTTGATTCAGAA 300
QY 101 TYrThrTYrPheCysAsnGlyLysIleIleAspLysArgLeuGlnGluLeuGlyAla 120
DB 301 TACACCTACTTTTGCATATGGGGGAGATATATGATTAACGACTTCACAGCTTGAGCC 360
QY 121 ArgHisPheTYrAspThrGlyHisAlaAspAspCysValGlyLeuGluLeuValGlu 140
DB 361 CGCATTTCTATGACACTGACATGCAGATGACGTGTAGTTAAGACTTGTGTTGAG 420
QY 141 ProThrIleAlaGlyLeuThrProAlaIleuArgLysHisPheArgSerSerArgGlyGln 160
DB 421 CCGTGATGCTGCTGACTGTGGCCGCTCAGAACCATTTTATGGTCAAGACAGACAA 480
QY 161 GluGluIleSerGlyAlaLeuProValAlaSerProAlaSerLeuArgThrAspLeuVal 180
DB 481 GAGGAGATAGTGCGCCACACTCCGGTGGCATCACCTGCATCCTTGAGGACAGACCTTGG 540
QY 181 LysSerGluLeuLeuHisIleGluSerGlnValGluLeuLeuArgPheAspAspSerGly 200
DB 541 AAGTCAGAGCTGTACACATGTAATCTCAAGTCAGACTTCTGATTCGTGATTCAGCA 600
QY 201 ArgLysAspSerGluValLeuLysGlnAsnAlaValAsnSerAsnGlnSerAsnValAl 220
DB 601 AGAAGGATTCAGGTTTGAAGCAAAATGCAAGTCAACGCAACCAATTCATGTTGTA 660
QY 221 IleGluAspPheGluSerSerLeuThrArgSerValProProLeuSerGlnAlaSerLeu 240
DB 661 ATTGAAGACTTTGAGTTCCTACCTTACCCGTCGTCGATCCACCTTCACAAAGCTCTCTG 720
QY 241 AsnIleProGlyLeuProProGluTYrLeuGlnValHisLeuGlnGluSerLeuGlyGln 260
DB 721 AATATTCTGTTTACCCGCCAGATAATTTACAGTACATCTGCAGAGAGTCTTGGCCAG 780
QY 261 GluGluSerGlnValSerValThrSerAlaAspProValPheGlnValProIleSerLys 280
DB 781 GAGGAAGCCAAATATCTGTGACTTCAGCATCCAGTTTTCAGTGCCAAATTTCAAG 840
QY 281 AlaValGlnLeuThrThrAsnAspAlaIleLysThrThrLeuLeuValGluLeuAspIle 300
DB 841 GCAGTTCAACTTACTAGATGATGATGCAATTAACCAACCACTGCTGGTGAATGGACATT 900
QY 301 SerAsnThrAspPheSerTYrGlnProGlyAspAlaPheSerValIleCysProAsnSer 320
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QY 321 AspSerGluValGlnSerLeuLeuGlnArgLeuGlnLeuGlnLysAspArgLysCys 340
DB 961 GATTCTGAGGTACCAAGCTCTCCAAAGCTCAGCTTGAATTAAGCAAGAGCAAGCTGC 1020
QY 341 ValLeuLeuLysIleLysAlaAspThrLysLysGlyValAlaThrLeuProGlnHisIle 360
DB 1021 GTCCCTTTTGAATAATAAGGACAGACACAAAGAGAGAGCTTACCCCGCATATA 1080
QY 361 ProAlaGlyCysSerLeuGlnPheIlePheThrTTPCysLeuGluIleArgAlaIlePro 380
DB 1081 CCGGCGGAGATGTTCTCTCCAGTTTCATTTTACCTGTGGTGTGAAATTCGAGCAATTCCT 1140

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QY 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgArg 400
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Db 1141 AAAAGGCATTTTGGAGCCCTGTGACATATACAGATGACAGTCTGAAAAGCCGACG 1200
QY 401 LeuGlnGluLeuGlySerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla 420
    |||
Db 1201 CTACAGAGGCTGTGACAGTAAACAAGGGGACCCGATTATATACCCCTTTGTACGAGATGCC 1260
QY 421 CysAlaCysLeuLeuAspLeuAlaPheProSerCysGlnProProLeuSerLeu 440
    |||
Db 1261 TGTGCTGCTGTGTGGATCTCTCTGCTTCCCTTCTTCCAGCCACCTCAGTCTC 1320
QY 441 LeuLeuGlnHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
    |||
Db 1321 CTGCTGAAACATCTTCTTAAACTTCAACCCAGACCATATTCGTGCAGCTCAAGTTTA 1380
QY 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
    |||
Db 1381 TTTTACCCAGGAAAGCTCCATTTTGTCTCAACATTTGTGAATTTCTGTCTACTGCCACA 1440
QY 481 ThrGluValLeuArgLysGlyValCysThrGlyTyrPheValLeuLeuValAlaSerVal 500
    |||
Db 1441 ACAGAGGTTCTGCGGAGGAGGAGTATGTACAGCTGGCTGGCTTGTGTGCTTCAAGTT 1500
QY 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
    |||
Db 1501 CTTTCAGCCAAACATACATGCATCCCATGAAAGACAGCGGAAGCCCTGGCTCTTACAGATA 1560
QY 521 SerIleSerProArgTyrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
    |||
Db 1561 TCCATCTCTCTCGAACACAAATCTTTCACATTACAGATGACCCCTCATCCCATC 1620
QY 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
    |||
Db 1621 ATATGTTGGGTCCAGGAGCGGACGATAGCCCGTTTATTTGGGTCTTACAAACATAGAGAG 1680
QY 561 LysLeuGlnGlnGlnHisProAspGlyAsnPheGlyAlaMetTyrLeuPhePheGlyCys 580
    |||
Db 1681 AAATCTCAAGAACACACCCAGATGAGAAATTTTGAGCAATGTGTGTTTGTGGCTGC 1740
QY 581 ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysGly 600
    |||
Db 1741 AGGCATTAAGATAGGATTTATCTATTTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGG 1800
QY 601 IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAla 620
    |||
Db 1801 ATCTTACTCATCTAAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGGAGAGCC 1860
QY 621 ProAlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnGlnValAlaArgIleLeu 640
    |||
Db 1861 CCAGCAAGATATGTACAAAGACATCATCTCATGTGCGCAGGTGGGAGAAATCTCTC 1920
QY 641 LeuGlnGlnAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspVal 660
    |||
Db 1921 CTCGAGGAGAACGGCCATTTATTTATGTGTGTGGAGATGCAAAAGAAATATGCGCAAGATGTA 1980
QY 661 HisAspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGluAlaMet 680
    |||
Db 1981 CATGATGCCCTTGTGCAAAATAATAGCAAAAGAGGTGTGAGTTGAAAACTAGAAGCAATG 2040
QY 681 LysThrLeuAlaThrLeuLysGluGluLysArgTyrLeuGlnAspIleTyrSer 698
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Db 2041 AAAACCTGGCCACTTAAAGAAAGAAAGAGCGTACCTTCAGATATTGTGTCA 2094
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Search completed: December 12, 2002, 08:26:03
Job time : 7 secs


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QY 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgArg 400
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Db 1141 AAAAAGCATTTTGGGAGCCCTTGAGACTATACAGTGCAGTGCCTGAAAGCCGAG 1200
QY 401 LeuGlnGluLeuYssSerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla 420
    |||
Db 1201 CTACAGAGGCTGTGCAAGTAACAAAGGGGACCGGATTAAGCCGCTTGTACGAGATGCC 1260
QY 421 CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
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QY 441 LeuLeuGlnHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
    |||
Db 1321 CTGCTGAAACATCTCTTAAACTTCAACCAGACCATATTGCTGCAAGCTCAAGTTTA 1380
QY 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
    |||
Db 1381 TTTCACCCAGGAAGCTCCATTGTTGCTTCAACATGTGTGSAATTTCTGTCTACTGCCACA 1440
QY 481 ThrGluValLeuArgLysGlyValCysThrGlyTyrPheValLeuLeuValAlaSerVal 500
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QY 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
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Db 1501 CTTACAGCAACATACATGATGATCCCATGAGACAGCGGAAAGCCCTGCTCCTAAGATA 1560
QY 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
    |||
Db 1561 TCCATCTCTCTGGAACAACTTTCTTCCACTTACAGATGATGACCCCTCAATCCCCTATC 1620
QY 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
    |||
Db 1621 ATATAGTGTGGTCCAGGAACCGCATAGCCCGCTTATTGGTTCCTACACATAGAGAG 1680
QY 561 LysLeuGlnGluGlnHisProAspGlyAsnPheGlyAlaMetIrrPheLeuPhePheGlyCys 580
    |||
Db 1681 AAACCTCAAGAACACACCCGATGGAAATTTGGAGCAATGTGTTTGTGGCTGC 1740
QY 581 ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGly 600
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QY 601 IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAla 620
    |||
Db 1801 ATCTTAACATCATCTAAAGCTTCTCTCTCAAGAGATGCTCTGTGGGGAGAGAAACC 1860
QY 621 ProAlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnIleValAlaArgIleLeu 640
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Db 1861 CCAGCAAGATATGTACAGACAAACATCCAGCTTCATGGCCAGCGGCGGAGAAATCCTC 1920
QY 641 LeuGlnGluAsnGlnHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspVal 660
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QY 661 HisAspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGluAlaMet 680
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Db 1981 CATGATGCCCTTGTGCAAAATATACCAAGAGGTTGGAAGTAAAAACTAGAACCATG 2040
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Db 2041 AAAACCTTGCGCCACTTTAAAGAAAGAAAGCGCTACCTTCAGATATTGTGTCA 2094
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Search completed: December 12, 2002, 08:27:19
Job time : 7 secs


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Db 1141 AAAAGGCAATTTTGGGAGCCCTGTGGACTATACAGTGCAGTGGTGAAGGCGCAGG 1200
QY 401 LeuGlnGluLeuLysSerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla 420
    |||||||
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QY 421 CysAlaCysLeuLeuAspLeuLeuValaPheProSerCysGlnProProLeuSerLeu 440
    |||||||
Db 1261 TGTGCTGCTGTGTGGATCTCTCTCGCTTCTTCCCTTCTTGCCAGCCACCTCAGTCTC 1320
QY 441 LeuLeuGlnHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
    |||||||
Db 1321 CTGCTGCAACATCTCTTAACCTTCAACCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
QY 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
    |||||||
Db 1381 TTTCACCCAGGAAGCTCCATTTTGTCTCAACATGTGGAATTTCTGTCTACTGCCACA 1440
QY 481 ThrGluValLeuArgLysGlyValCysThrGlyTyrLeuAlaLeuValAlaSerVal 500
    |||||||
Db 1441 ACAGAGGTTTGGGGAAGGAGGATGTACAGGCTGGCTGTGTGTGCTTCAAGTT 1500
QY 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
    |||||||
Db 1501 CTTACAGCAACATACATCATGATCCCATGAGACAGCGGAAGCCCTGGCTCCTAAGATA 1560
QY 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
    |||||||
Db 1561 TCCATCTCTCTCGAACACAAATCTTTCTTCCATGATGATGATGATGATGATGATGATG 1620
QY 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
    |||||||
Db 1621 ATATATGTTGGTCCAGGACACCGCATAGCCCGCTTATTTGGTTCCTACACATAGAGAG 1680
QY 561 LysLeuGlnGluGlnHisProAspGlyAsnPheGlyAlaMetTyrPhePheGlyCysArg 580
    |||||||
Db 1681 AAATCCAAAGAACACACCCAGATGGAATTTTGGAGCAATGTGGTGTGGCTGCAGG 1740
QY 581 HisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGlyIle 600
    |||||||
Db 1741 CATAGGATAGGGATTAATCTATTCAGAAAGACCTCAGACATTTCTTAAGCATGGGATC 1800
QY 601 LeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGlnGluAlaPro 620
    |||||||
Db 1801 TTAACTCATCTAAAGTTCTCTCTCAGAGATGCTCTCTGTGGGAGGAGAGCCCA 1860
QY 621 AlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnIleValAlaArgIleLeuLeu 640
    |||||||
Db 1861 GCAAGATATGTACAGACACATCCAGCTTCATGGCCAGAGTGGCGAGATCTCTCTC 1920
QY 641 GlnGlnAsnGlnHisIleTyrValLysGlyAspAlaLysAsnMetAlaLysAspValHis 660
    |||||||
Db 1921 CAGGAGAACGGCCATATTATGTGTGTGAGATGCAAAAGATATGGCCAGAGATGTACAT 1980
QY 661 AspAlaLeuValGlnIleIleSerLysGluValGlyValGlnLysLeuGlnAlaMetLys 680
    |||||||
Db 1981 GATGCCCTTGTGCAATTAATACCAAGAGTGTGAGTTCAAAAACATAGAACATGAAA 2040
QY 681 ThrLeuAlaThrLeuLysGlnGluLysArgTyrLeuGlnAspIleTyrSer 697
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Db 2041 ACCCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAGAGATATTGGTCA 2091
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Search completed: December 12, 2002, 08:28:29
Job time : 4 secs

QY 381 LysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgArgLeu 400
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Db 1144 AAGGCAATTTTGGAGCCCTTGGACTATACAGTACAGTGTCTGAAGAAGCCAGGCTA 1203
QY 401 GlnGluLeuCysSerIysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAlaCys 420
|||||
Db 1204 CAGGAGCTGTGCATTAACAGAGGGGAGCCGATTAAGCCGCTTGTACGAGATGCCGTG 1263
QY 421 AlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeuLeu 440
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Db 1264 GCCTGCTTGTGGATCTCTCTCCGCTTCCCTTCCCTTCCAGCCACCTCACTCACTCTCTG 1323
QY 441 LeuGlnHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeuPhe 460
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Db 1324 CTCGACATCTTCTTAACCTTCAACCCAGACCATATTCGTGCAAGCTCAAGTTATTTT 1383
QY 461 HisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThrThr 480
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Db 1384 CACCCAGGAAGCTCCATTTTGTCTCAACATGTGGAATTTCTGTCTACTGCCACACA 1443
QY 481 GluValLeuArgLysGlyValCysThrGlyTyrPheAlaLeuLeuValAlaSerValLeu 500
|||||
Db 1444 GAGGTTCTGCGGAGAGGAGTATGTACAGCTGCGTGGCTTGTGTGCTTCACTTCTT 1503
QY 501 GlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIleSer 520
|||||
Db 1504 CAGCCAAACATACATCATGCCATGGAAGAGAGGAGAAAGCCCTGGCTCTTAAGATATCC 1563
QY 521 IleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIleIle 540
|||||
Db 1564 ATCTCTCTCGAACAACAAATCTTTCACATCACAGATGACCCCTCAATCCCATCATA 1623
QY 541 MetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgAsnSer 560
|||||
Db 1624 ATGGTGGGTCCAGAGAACCGGACGAGCCGCTTATTTGGGTCTTACACATAGAAACTCC 1683
QY 561 LysAsnAsnThrGlnMetGluLeuGlnGlnCysGlyCysPheLeuAlaAlaGlyIle 580
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Db 1684 AAGAACACACACCAGATGGAATTTTGGAGCAATGTGTTGTTTGGCTGCAGGCATA 1743
QY 581 ArgIleGlyIleIleTyrSerGluLysSerSerAspIleSerLeuSerMetGlySer--- 599
|||||
Db 1744 AGGATAGGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGGATCTTA 1803
QY 600 LeuIle---ArgPheProSerGlnGluMetLeuLeuGlnIleArgArgLysProGlnGln 618
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Db 1804 CTCATCTAAAGTTTCTCTCTCAGAGATGCTCTGTGGGAGAGAGAAAGCCCAACAA 1863
QY 619 SerMetTyrLysThrThrSerSerPheMetAlaSerArgTyrArgGluSerSerSerArg 638
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Db 1864 AGTATGTACAGACACATCCAGCTTCATGGCCAGAGGTGGGAGAGATCCTCTCCAGG 1923
QY 639 ArgThrAlaIlePheMetCysValGluMetGlnArgIleTyrProArgMetTyrMetMet 658
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Db 1924 AGAACGGCCATATTTATGTGTGTGAGATGCAAAAGATATGGCCAAAGATGTACATGATG 1983
QY 659 ProLeuCysLys-----AlaLysArgLeuGluLeuLysAsn---LysGln---LysPro 674
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Db 1984 CCTTGTGCATAATTAATAGCAAAAGAGGTGGAGTTGAAAATACTAGAAACATGAAAAACC 2043
QY 675 TyrProLeu---LysLysLysAsnAlaThrPheArgIlePheGlyHis 689
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Db 2044 TGGCCACTTTAAAGAGAAAACGCTACCTTCAGAGATATTGCTCAT 2091

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Job time : 6 secs